

APPENDIX A

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Introduction

The main purpose of the generic matcher tool is to allow for the comparison of two different sets of objects based on their common attributes. For this purpose the generic matcher provides a user friendly GUI, presenting the user with total control over how and what is matched. The objects are compared on the basis of attributes of the source object. It is helpful to go over some terms used when talking about generic matcher. The class/concept containing objects that are being compared is referred to as the source class, whereas the class containing the objects against which the source objects are being compared is referred to as the target class. The source and target class must be part of the same ontology. Match criteria is a set of tuples for each source attribute being compared. A tuple in this case contains the source attribute, the target attribute it is being compared to (can be null), the matching function being used to facilitate the comparison and the weight associated with this attribute.

Step 1: Starting up the matcher

Before starting up the generic matcher you want to make sure that you java and xsb are part of your path. To start up the matcher you need to execute the runMatcherMain.bat file located in generic_matcher folder.

Step 2: Loading an ontology

Next we need to load ontology into matcher. You can do this by using the “Load OMS” menu item in located in the file menu. This command removes any previously loaded OMS and loads in the new OMS. If you do not want to unload the previous OMS you can use the “Merge OMS” command. Other options available in this menu allow you to save the OMS. By saving the OMS you are also saving any match criteria you may have added or modified. The “Save OMS Schema” command lets you save the only the schema part of the OMS, this includes concepts, relationships and match criteria objects.

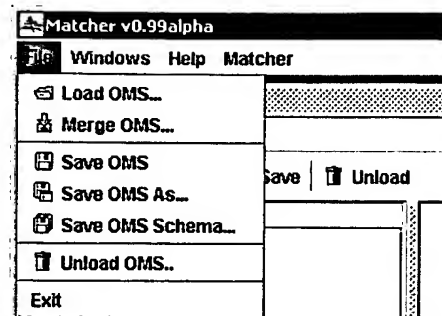


Fig. 1 Matcher File Menu

Step 3: Choosing Source/Target Classes

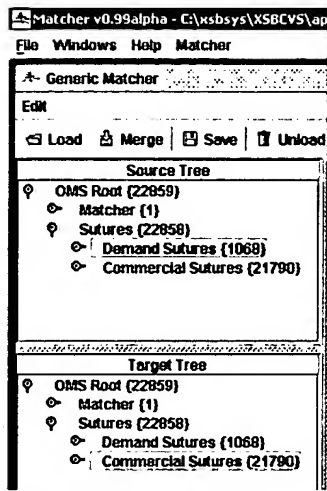


Fig. 2 Source/Target Trees

Once an OMS has been loaded we can go ahead and choose the source and target classes. The source class is chosen from the top tree and the target class is in the bottom tree. The number next to the name of the class is the number of objects that are members of this class. You can also view the relationships associated with this class by right clicking on the node and choosing the "View Relationships" option. You should notice some of the other options that are available when you right click on a node. These include the ability to import objects form a batch file or database table. The user also has the ability to add new classes and relationship under this node. Once you have chosen both the target and source attribute the right panel of the main window will be rendered. At this point the matcher will try to find a stored default match criteria for these two classes. If it is found its settings will be displayed, otherwise the matcher

will create a new default match criteria.

Step 4: Managing match criteria

Source Class : Sutures Target Class : Commercial Sutures

Sutures:Commercial Sutures Add Remove

Current Match Settings: Sutures:Commercial Sutures:Default

Source Relationships	Target Relationships	Matching Functions	Weight
AMDF-USER PACKAGE IN	AMDF-USER PACKAGI	Equals	x 1.0
ARMED SUTURE NEEDLE	ARMED SUTURE NEED	Equals	x 1.0
SUTURE NEEDLE STYLE	ARMED SUTURE NEED	Equals	x 1.0
COLOR	COLOR	Equals	x 1.0
DIAMETER	DIAMETER	Equals	x 1.0
Description String	Description String	Equals	x 1.0
END TYPE	END TYPE	Equals	x 1.0
EYE STYLE	EYE STYLE	Equals	x 1.0
FIGURE NUMBER	FIGURE NUMBER	Equals	x 1.0
IGNORE	IGNORE	Equals	x 1.0
ITEM NAME	ITEM NAME	Equals	x 1.0
LENGTH	LENGTH	Equals	x 1.0
MANUFACTURER	MANUFACTURER	Equals	x 1.0

Score Cutoff: 0.0

Select Objects To Match

Fig. 3 Right Panel

The right panel is composed of three different components.

1. Here the user can create and delete match criteria. The user can also choose from the different match criteria associated with this pair of source and target classes. All pairs of source and target classes have a default match criteria associated with them. The default criteria can be modified but cannot be deleted.
 - a. Add Button: Creates a copy of the current match criterion and adds it to the drop down box. Once the button is clicked the matcher will ask you to name the new criteria. Once the match criterion has been named it will be set as the selected criteria in the drop down box. When a new match criterion is created the settings of the previous criterion are copied into the new one.
 - b. Remove Button: Deletes the currently selected match criterion in the drop down box. Remember you cannot delete the default match criteria.
 - c. Drop down Box: Displays the currently selected match criteria. The settings associated with this match criteria are displayed in the part 2 of the right panel. To change the match criteria just select it from the drop down box.
2. In this part of the right panel the settings associated with the currently selected match criterion are displayed. There are four columns: Source relationship, Target Relationship, Matching Function and Weight.
 - a. Source Relationship: Relationship associated with the source class
 - b. Target Relationship: Relationships from the target class are of the same type as the source relationship. The user can choose from any one of the different choices available in the drop down box. If you don't want this relationship to be compared you can set the value to null.
 - c. Matching Function: Here we can choose from the different matching functions available to compare the data type associated with this relationship.

- d. **Weight:** Weights provide a way to increase the emphasis on a particular attribute.
- 3. The third part of this panel contains the score cutoff and the match button
 - a. **Score Cutoff:** The score cutoff value determines what match results are returned. Match results which have a score greater than or equal to the score cutoff will be returned.
 - b. **Select objects to match:** Once the match criterion has been set you can start the match process by pressing this button. When the button is pressed a window displaying all objects under the source class will be displayed.

Step 5: Selecting objects to match

The object chooser window displays all the objects under the source class. The name and native id of these objects are displayed. You can choose any number of objects to compare or you can select all the objects are under the class. To select multiple objects use the CTRL and SHIFT keys to select contiguous and noncontiguous objects. To match only the selected objects click on the “Match Selected Objects” button or to match all objects click on the “Match All objects button.

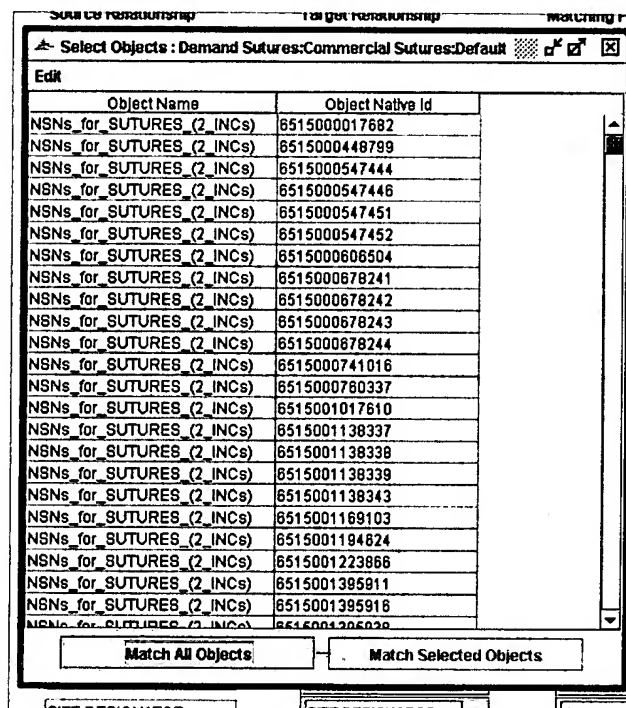
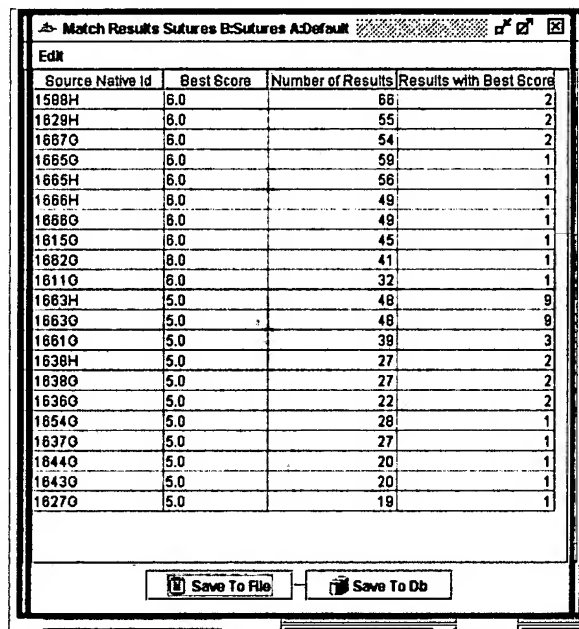


Fig. 4 Object Chooser

Step 6: Match Results

The match results windows will show all matches above the cutoff. Four different columns are displayed in this window: the native id of the source object that was matched, the best score attained when matching this object, the number of target objects that matched and the number of target objects that attained the highest score. At this point the user has several options. One option is so to save the results to either a flat file or a database. This can be done by clicking on the respective buttons located at the bottom of the window. Another option is to view in detail the matches associated with one of the source objects. To bring up the detail results window right click on the source object and select the "View All Matching Target Objects" option.



The screenshot shows a window titled "Match Results Sutures B:Sutures A:Default". It contains a table with four columns: "Source Native Id", "Best Score", "Number of Results", and "Results with Best Score". The table lists 30 source objects with their respective scores and counts. At the bottom of the window, there are two buttons: "Save To File" and "Save To Db".

Source Native Id	Best Score	Number of Results	Results with Best Score
1598H	6.0	66	2
1629H	6.0	55	2
1687O	6.0	54	2
1665O	6.0	59	1
1665H	6.0	56	1
1666H	6.0	49	1
1666O	6.0	49	1
1615O	6.0	45	1
1682O	6.0	41	1
1611O	6.0	32	1
1683H	5.0	48	9
1663O	5.0	48	9
1661O	5.0	39	3
1638H	5.0	27	2
1638O	5.0	27	2
1636O	5.0	22	2
1654O	5.0	28	1
1637O	5.0	27	1
1644O	5.0	20	1
1643O	5.0	20	1
1627O	5.0	19	1

Fig. 5 Match results window

Step 7: Detail Results Window

Like the right panel in the main window before the detail results window is also composed of the three distinct parts.

1. The top part of the window is used to display information about the source object you have selected. The name of the attributes, their values and the weights associated with each are displayed. The highest possible score that can be achieved taking into account the weights is shown in the last line; in this case it is equal to 9.0.
2. The main part of the window displays the target objects that matched the source object, the total score of the match along with the values of attributes associated with the target objects. A color coding scheme is used to distinguish between values that were compared and matched, were compared and didn't match, and those that were not compared.

In this particular example the color green is associated with values that were compared and matched. So for example if you take a look at the length attribute of the highlighted example both the source and target objects have a length of 18.0 inches. The second value in this cell [1.0000] is the score associated with this match. This is equal to the value returned by the matching function (matching functions always return a value between -1.0 and 1.0) multiplied by the weight entered for the source relationship.

Source Class : Batch-ESUR0_HARVEST
Source Object : 16650

ARMED SUTURE NEEDLE POINT STYLE : REVERSE CUTTING EDGE : 1.0
ARMED SUTURE NEEDLE STYLE : 3/8 CIRCLE : 1.0
LENGTH : 18.0 INCHES NOMINAL : 1.0
STRAND FIBER ARRANGEMENT : MONOFILAMENT : 1.0
COLOR : BLACK : 1.0
SIZE DESIGNATOR : 8-0 : 1.0
MATERIAL AND LOCATION : NYLON : 1.0
ITEM NAME : RE, NONABSORBABLE, SURGICAL : 1.0
NEEDLE TYPE DESIGNATOR : P3-3 : 1.0
Weights Total : Highest possible score : 9.0

Score	Target Object	COLOR	ITEM NAME	LENGTH	MATERIAL AN...	NEEDLE DESIGN	NEEDLE TYP...	SIZE DESIGN
1.0	851501055022 3	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY	P-3	8-0
1.0	851501055022	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY	P-3	8-0
1.0	851501054426 3E	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	CUTICULAR		8-0
1.0	851501045443 3	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	SUTUPAK		8-0
1.0	851501045443	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	SUTUPAK		8-0
1.0	851501040081 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851501040081	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500982715 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500987698 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500944987 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500944987	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500917583 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500917583	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500905147 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500905147	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0
1.0	851500823784 12	BLACK	RE, NONABSORBABLE, SURGICAL	18.0 INCHES NOMINAL	NYLON	PLASTIC SURGERY		8-0

Match : No Comparison : No Match :
green yellow red

Fig. 6 Detail results window

The color red is associated with values that were compared but did not match. Again looking at the highlighted example it is clear to see that the source and target object values for the “Needle Type Designator” attribute don’t match.

If the target object has a populated value for an attribute, in this case let’s look at the “Needle Designator” attribute. By looking at the attributes linked to the source object we can see that this attribute does not exist. In this case no comparison occurs and this cell is colored gray and the value of the target attribute is displayed with no score. If the reverse happens and the source object has a value and the target object does not as is the case for “Color” attribute, the corresponding cell is left empty and colored gray.

It is often the case that for an attribute a target object may have multiple values. When this occurs a second row for the object is inserted into the table and the whole row is colored white as is the case in the highlighted example. One of these values is matched to by the matcher and the appropriate coloring is used. In this case the second value is compared and a score of [-1.0000] is assigned.

3. The colors used for these different situations can be changed at any time by using the drop down boxes in section 3 of the window. They can also be changed using the “Set Colors” menu item located in the “Matcher” menu in the main window.

Step 9: Saving results

As mentioned before the user has the option to save match results to a file or database. When saving to a file the generic matcher saves a table similar to the one displayed in the detail results window to flat bar separated text file. For each source object a table is constructed similar to the one displayed in the results window and saved into the file. The file contains the tables for all the source objects that were matched.

When saving to a database a similar action is performed. It is important to note a couple of things about saving results to a database. When the feature is first activated the user will be asked to specify the location of a preexisting access database file. Next the user will be asked for the name of the database table where the results will be saved. If the table does not exist it will be created. If a table by the name already specified already exists and the structure is the same as that needed to save the results the table will be appended. The columns of the table are same as those in the detail results window with one added to specify the source object being matched.

Importing Objects into the OMS

The generic matcher provides the ability to import objects from either a file or database. To start the process right click on the node under which you want the objects inserted. Select the "Import Objects from File/Db" option; this will open a file directory browser allowing the User to select the desired batch file or access database file from their file directory. Navigate through the directory structure to locate the desired batch file or database and select the batch file to be loaded and select the "Import" button.

If the user selects a database ".mdb" file the user will be asked to enter the name of the database table from which to import the objects. Otherwise the User will be prompted to select a column delimiter for the batch text file to be loaded into the Matcher. The User will have the option of choosing from pipe, comma, colon, and tab as possible file delimiters. Once the appropriate delimiter has been selected, the User should select the OK button to prompt the Matcher to load the batch file. (See Fig 7)

An editor will now be displayed, allowing the User to select which columns of the batch file or fields from the database table they want imported. Under the First Line/Title heading, the User will see a list of all of the names or titles of the columns in the text file (It is assumed that first row of the file contains column names separated by a pre-selected file delimiter). The user will now need to select appropriate designations for each of these columns from the drop down list found under the Relationships heading. The Relationship designations for each column are essentially a set of instructions on how the Matcher should handle the information contained within the column. To select a Relationship designation for an attribute, the User must triple click on the drop down box in the Relationships column and select one of the options displayed.

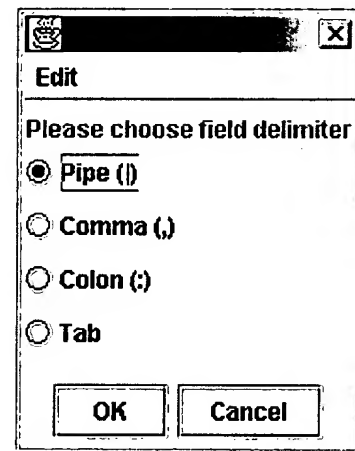


Fig 7 Text file delimiters

First Line/Title	Relationships	Options
MFG ITEM ID	Description	
VENDOR ITEM ID	ID	
MFG ID	Description	
SITE	Ignore	
DESCRIPTION	Sample Description	
DESCRIPTION	Description	

OK Cancel

Fig. 8 Object extractor settings

A brief description of some of the extractor options available for the User to choose from in the Relationships column are provided below for reference:

- **Id** - One of the columns has to contain a unique identifier for each description. This will help User to relate extracted attributes to the description provided. Choosing the ID option for that column will tell extractor that that column contains unique identifiers. It is important to note that no more than one attribute should contain the ID relationship identifier but it is not necessary that any of the attributes contain the ID identifier.
- **Description** – Tells the extractor to load this column as a description. The User can choose several columns to be loaded as descriptions. They will be concatenated to each other.
- **Ignore** – Tells the extractor not to load this column.

Other designations may be displayed in the Relationships window drop down box; in choosing them the User specifies that the values of the text column should be directly loaded as attributes of the objects for the corresponding designation names.

After selecting the appropriate designations from the Relationships column, the User will also be able to select from one of three possible options for each attribute in the

Options Column. The User will be able to prompt the extractor to append the title in front of or behind or ignore the title for each attribute extracted. (See Fig 9)

First Line/Title	Relationships	Options
MFG ITEM ID	Description	
VENDOR ITEM ID	ID	Append Title in Front
MFG ID	Description	Append Title in Front Append Title After Ignore Title
SITE	Ignore	
DESCRIPTION	Description	

OK Cancel

Fig. 9 Object extractor options

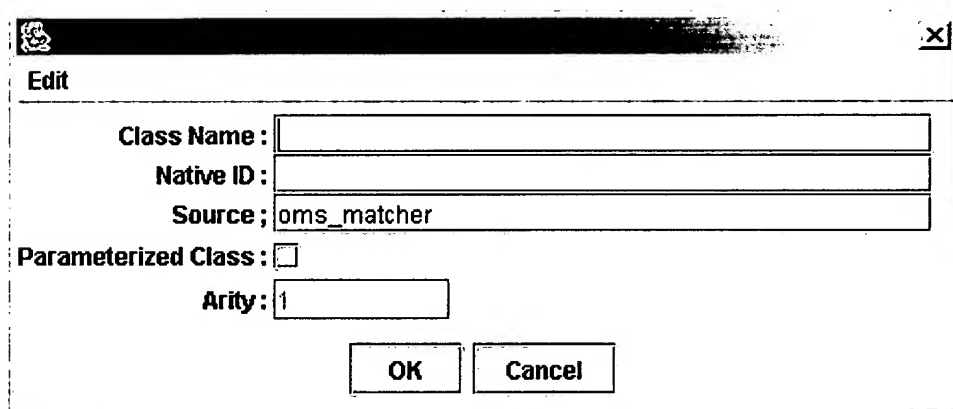
For example, if one of the columns in the imported text has a title *USABLE_LENGTH* and that column contains only measures (like 4") and the User prompts the extractor to ignore the title, the description will be displayed as 4". If the User prompts the extractor to append the title in front, the information reported back to the User will be *USABLE_LENGTH* 4", and if the User opts to have the title appended after, the information will be presented back as 4" *USABLE_LENGTH*.

Once the User has configured all of the necessary options, they must click on the OK button to load the batch into the OMS. If the batch was loaded successfully a new node will appear under the selected node containing all the imported objects. The number of objects imported will also be displayed next to the name of the new node.

Adding a new class

The generic matcher provides some rudimentary OMS editing functions. One of these is the ability to add a new class to the OMS. To add a class, select the class, under which you want the new class to appear, right click and choose the “Modify OMS/Add a new Class” option from the pop up menu. A dialog appears allowing the user to enter the name, native id and source of the new class. You also have the option to make the new class a parameterized class. This is done by checking the box next to the “Parameterized Class” label and entering the arity of the class below it. If the new class is a parameterized class the use will be prompted to choose from the existing concepts in the OMS the arguments of the class.

If the class was added successfully it will appear under the parent node when you click ok.

The image shows a Windows-style dialog box titled "Edit". It contains several input fields and a checkbox. The "Class Name" field is empty. The "Native ID" field is empty. The "Source" field contains the text "oms_matcher". The "Parameterized Class" checkbox is unchecked. Below it, the "Arity" field contains the number "1". At the bottom right, there are two buttons: "OK" and "Cancel".

Edit

Class Name :

Native ID :

Source :

Parameterized Class : ☐

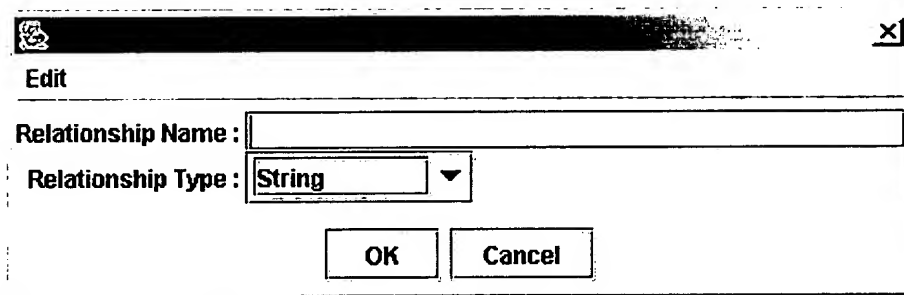
Arity :

OK **Cancel**

Fig.10 New class dialog.

Adding a new relationship

Along with the ability to add a new class to the OMS generic matcher provides the ability to add relationships to the class. To start this process select the class you want to modify, right click on the node and select the “Modify OMS/Add a new Relationship” option. A dialog box will appear where you must enter the name of the new relationship. The user must also specify the type of the relationship, i.e. what type of values will this relationship have e.g. string, number, measure etc. To verify whether the new relationship was added properly you can always view the relationships attached to a class by right clicking on the node and selecting the “View Relationship” option.



The image shows a software dialog box titled "Edit" with a close button in the top right corner. Inside the dialog, there are two labeled input fields. The first is "Relationship Name:" followed by a text input box. The second is "Relationship Type:" followed by a dropdown menu that currently displays "String". At the bottom of the dialog, there are two buttons: "OK" and "Cancel".

Fig. 11 New Relationship Dialog

Editing user preferences

Generic matcher provides a central location where preferences can be managed. To edit preferences select the “Edit Preferences” menu item under the “Matcher” menu. A dialog box should appear listing the various options that can be set. Once you have set all the options simply close the dialog box. All the user specified preferences are saved in the prefs file located in the application directory; it is recommended that the user not edit this file.

- **OMS Load Dir:** This is the directory to which matcher opens the file dialog when the user uses the load or merge options.
- **OMS Startup Dir:** The user can specify for an OMS to be loaded by default each time the matcher starts up.
- **Previous Match Results:** Whenever a match is executed in the generic matcher information regarding scores is added to the oms as an attribute of the source object. If you wish not to save this information choose this option. It is important to note that this option causes adverse effects if any result windows are open when saving occurs.
- **Scoring Information:** By default when matcher saves match results the individual scores assigned to object attributes are not saved. If the user chooses this option the scoring information will be saved along with the attribute values.
- **Maximize @Startup:** Option to maximize the window at startup.
- **Hide System Nodes:** Option to hide class nodes in the source and target trees for concepts that have a system source, e.g. oms, tms, ode, odc etc. .

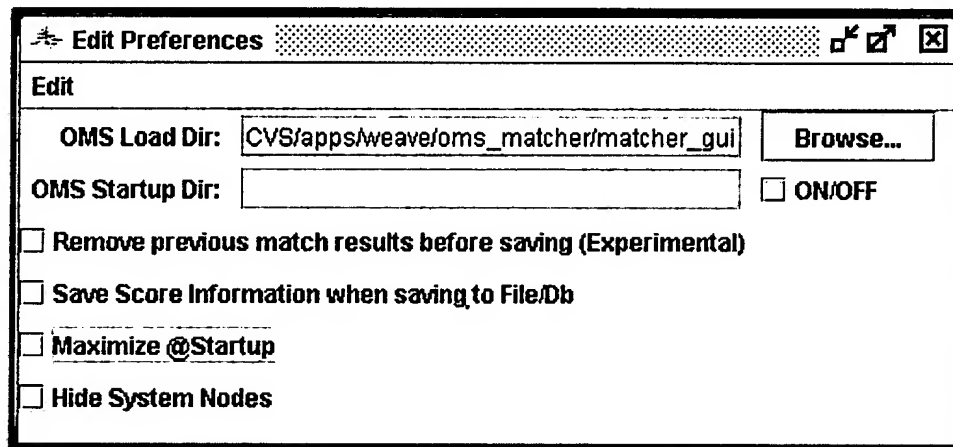


Fig. 12 Edit preferences dialog.

Another selection available under the “Matcher” menu is the option to “Write Results directly to file.” When this option is selected the results window will not appear when a match is completed instead the user will be asked whether he/she wants to save the results to a file or a database.

Help Browser

Generic matcher provides built in help features including the help browser. The help browser allows the user to view application documentation and see answers to frequently asked questions. To invoke the help browser simply click on the “Help Contents” menu item under the “Help” menu. The help browser is very similar to an internet browser and provides quick answers to questions.

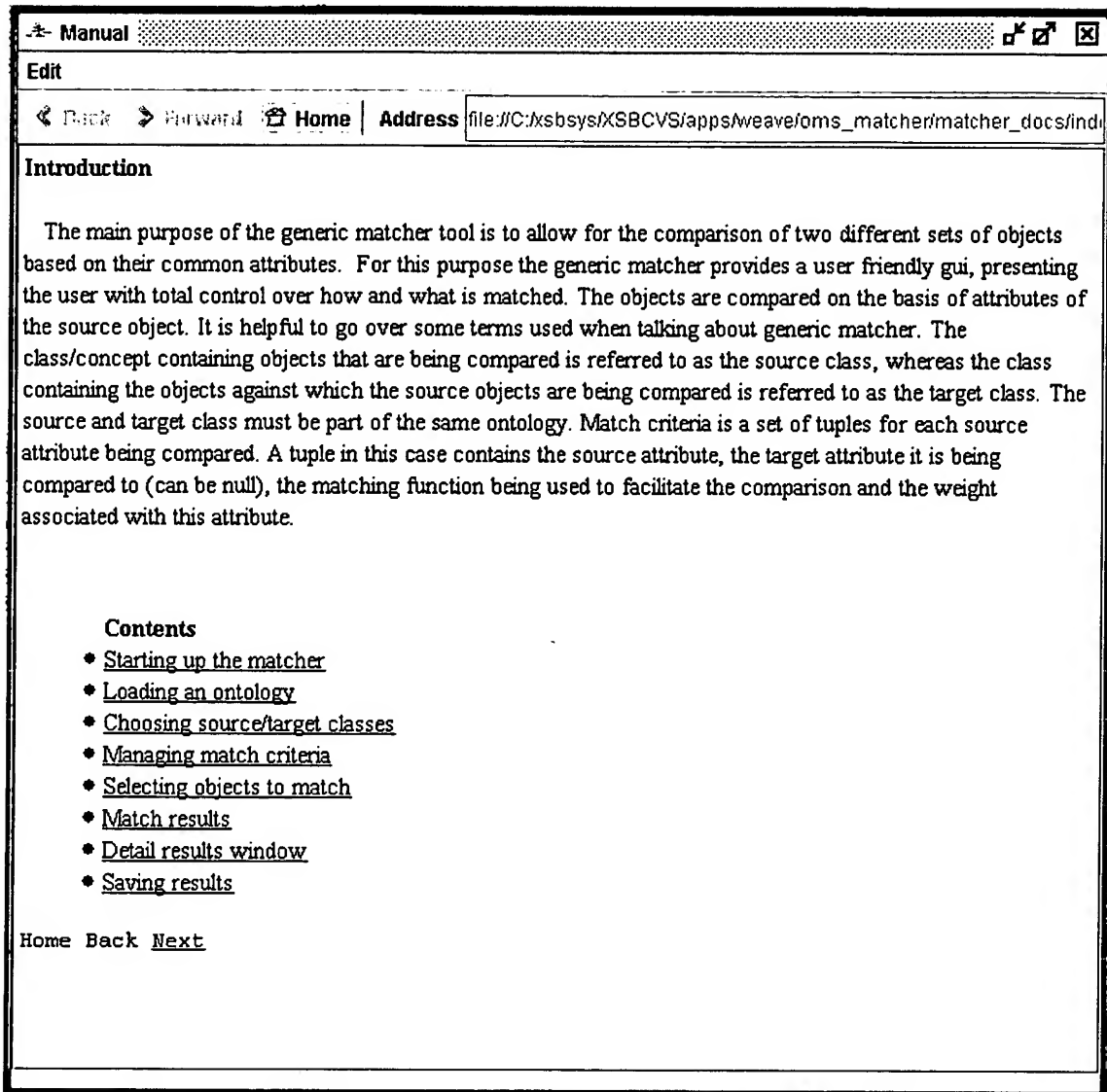


Fig. 13 Help Browser

Matching function descriptions

To view a description about the available matching functions, along with how they handle scoring click on the “Function Descriptions” menu item under the “Help Menu.” This feature provides information about every matching function that is currently shipped with matcher and have been loaded.

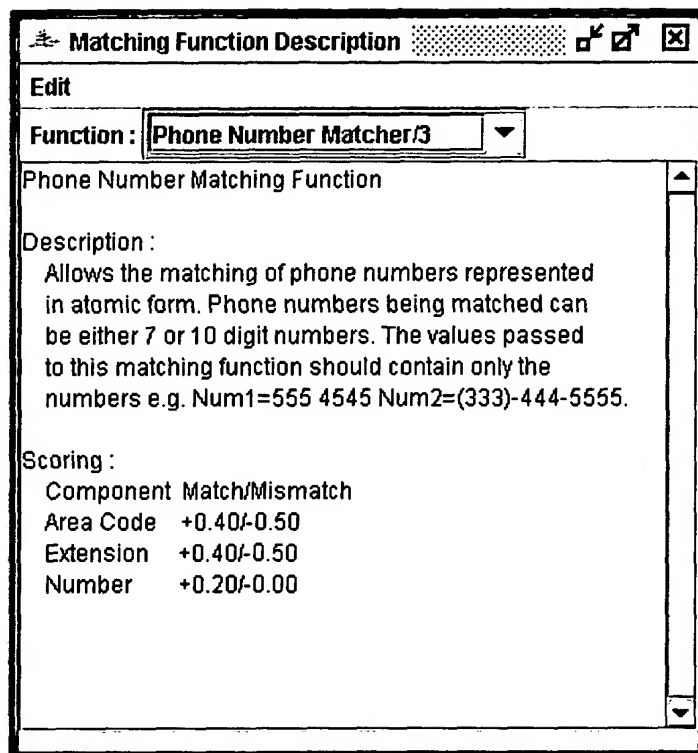


Fig. 14 Matching function descriptions.

A - Glossary:

Class - (sometimes referred to as a node or a concept) a set containing members regarded as having certain relationships in common, a kind or category.

Match Criterion – the source and target class, the set of attributes being compared, the weights and matching function associated with each attribute and the score cutoff all together form the match criterion.

Matching Function – specialized prolog predicate used by the matcher to compare two values of a particular data type. Matching functions always return a value between $[-1.0, +1.0]$.

OMS - ontology management system to manage and store ontology-based knowledge.

Parameterized Class – represents an infinite set of Values such as integers, measures and so on. For example, number of sutures in a package may be any integer – we can not name all of the possible Values.

Source Class – is the class in the ontology containing the set of objects that are currently being compared.

Target Class – is the class in the ontology containing the set of objects that the source objects are being compared against.

Source Object – is a member of the source class.

Target Object – is a member of the target class.